

**Table 4.** Differential expression of Apo E isoforms in AD patients versus contrast groups.

Apo E NPI	pI	MW (kDa)	6 AD vs. 6 D	6 AD vs. 10 FTD	6 AD vs. 6 FTD	6 AD vs. 4 VAD	Aa # start-end	Peptide sequence #	Seq ID No.
34	5.11	35.2	↓	=	=	=	270-278	LQAEAFQAR	1
							259-269	AKLEEQQQQIR	2
							166-175	LLRDADDLQK	3
							19-33	KVEQAVETEPEPELR	4
35	5.32	34.3	↓	nd	nd	nd	270-278	LQAEAFQAR	1
							259-269	AKLEEQQQQIR	2
							199-207	GPLVQEGR	5
							301-317 (C-term.)	VQAAVGTSAAAPVPSDNH	6
72	5.07	15.8	=	=	nd	nd	199-207	GPLVQEGR	5
							270-278	LQAEAFQAR	1
							259-269	AKLEEQQQQIR	2
							270-278	LQAEAFQAR	1
73	5.11	15.8	=	=	=	=	199-207	GPLVQEGR	5
74	4.91	15.8	=	=	=	↓	270-278	LQAEAFQAR	1
							259-269	AKLEEQQQQIR	2
							210-224	AATVGSLAGQPLQER	7
							138-152	GEVQAMLGQSTEELR	8
							94-108	SELEEQLTTPVAEETR	9
							301-317 (C-term.)	VQAAVGTSAAAPVPSDNH	6
75	5.09	15.1	=	nd	nd	nd	138-152	GEVQAMLGQSTEELR	8
							19-33	KVEQAVETEPEPELR	4
							270-278	LQAEAFQAR	1
							19-33	KVEQAVETEPEPELR	4
41	5.07	15.3	↓	nd	nd	nd	270-278	LQAEAFQAR	1
							210-224	AATVGSLAGQPLQER	7
							259-269	AKLEEQQQQIR	2
76	5.24	13.8	= $\downarrow$	↓	=	↓	270-278	LQAEAFQAR	1
77	4.96	12.4	= $\uparrow$	=	=	=	210-224	AATVGSLAGQPLQER	7
52	5.30	33.8	↓	nd	nd	nd	270-278	AKLEEQQQQIR	2
							270-278	LQAEAFQAR	1

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								199-207 259-269	5
60	5.38	15.6		nd	nd	nd	nd	AKLEEQQQIR	2
66	5.17	30.	↓QL	nd	nd	nd	nd	ALMDETMKELK KVEQAVETEPEPELRL LGPLVEQGR AYKSELLEQLTPVAEETR LSKELQAAQAR AATVGSLAGQPLQER AKLEEQQQIR LQAEAFQAR KVEQAVETEPEPELRL AYKSELLEQLTPVAEETR LSKELQAAQAR AATVGSLAGQPLQER AKLEEQQQIR LQAEAFQAR	10 4 5 11 12 7 2 1 4 11 12 7 2 1
								199-207 259-269 80-90 19-33 199-207 91-109 111-121 210-224 259-269 270-278 19-33 91-109 111-121 210-224 259-269 270-278	
11	5.22	35.3	nd	↓QL	nd	nd	nd	GPLVEQGR AKLEEQQQIR AATVGSLAGQPLQER LQAEAFQAR KVEQAVETEPEPELRL AYKSELLEQLTPVAEETR LSKELQAAQAR AATVGSLAGQPLQER AKLEEQQQIR LQAEAFQAR	
									1

Only quantitative results are showed (with the exception of NPI 66 and NPI 11, where only a qualitative difference (QL) was found).

↓: down-regulated in AD {↓: p<0.05; =↓: p < 0.07}

↑: upregulated in AD {↑: p<0.05; =↑: p<0.07}

=: no significant difference

#: peptide sequences covered by MS analysis

nd: not detected

**Table 5.** Identification of the protein spots that were altered between the studied groups.

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Spot exp1	Spot exp2	Peptide	Seq ID No. aa	Identification in database	ID number database
4705 7206	355	AVLTIDEK LGMFNQIQHCK (Cys-CAM) QNDYVEK LSITGTYDLK SVLGQLGITK VFSNNGADLSGVTEEAPLK LLELTGPK ATWSGAVLAGR FALVREDR CLAPLEGAR (cys-CAM + ox) FALVREDR LETPDFQLFK ATWSGAVLAGR LLELTGPK EVPLNTIHFMGR + 1 Oxidation (M) DVVSQFEGSALGK VQPYLDDFQK [9 6.56] <sup>†</sup> ALKED[360.25] <sup>†</sup> (aa 208 : N → D) ATEHLSTLSEK AKPALEDLR LSPLGEEMR + 1 Oxidation (M)	27 29 17 24 24 25 26 30 31 32 33 32 34 31 30 36 35 36 37 38 39 40 41 42 43 44 45 46 47 36	360-367 248-257 180-187 315-324 325-334 335-352 86-93 386-396 313-320 304-312 313-320 32-41 386-396 86-93 446-457 52-64 121-130 201-212 220-230 231-239 165-173 185-195 70-83 48-64 202-212 240-250 143-155 52-64 Apolipoprotein A-I	P01009 P01009 Alpha-1-antitrypsin Alpha-1-antitrypsin P04217 P04217 Alpha-1B-glycoprotein Alpha-1B-glycoprotein P04217 Alpha-1B-glycoprotein P04217 Alpha-1B-glycoprotein P04217 Antithrombin-III Apolipoprotein A-I P01008 P02647 P02647
4801RBH 4803	375				
1RBH					
901RBH					
5702 6102	149				
6303	146				

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Spot exp1	Spot exp2	Peptide	Seq ID No. aa	Identification in database	ID number database
		VQPYLDDFQK [916.56] <sup>+</sup> ALKED[360.27] <sup>+</sup> (aa208 : N → D)	37	121-130	
		ATEHLSTLSEK	38	201-212	
		LSPLGEEMRDR + 1 Oxidation (M)	39	220-230	
		LSPLGEEMR + 1 Oxidation (M)	48	165-175	
		THLAPYSDEL R	41	165-173	
		DSGRDYYVSQFEGSALGK	42	185-195	
		DYVSQFEGSALGK	44	48-64	Apolipoprotein A-I
			36	52-64	P02647
7101	285	[1315.83] <sup>+</sup> DNDDDSVTSTFSK (aa 74: W → D) QEMSKDLEEVK + 1 Oxidation (M)	49	70-83	
		VQPYLDDFQK	50	108-118	
		VQPYLDDFQKK	37	121-130	
		LSPLGEEMR + 1 Oxidation (M)	51	121-131	
		LSPLGEEMRDR + 1 Oxidation (M)	41	165-173	
		THLAPYSDEL R	48	165-175	
		LEALKED[360.25] <sup>+</sup> (aa 208 : N → D)	42	185-195	
		LEALKENG GAR	52	202-212	
		ATEHLSTLSEK	45	202-212	
		AKPALEDLR	39	220-230	
		DLATVYVDVLK	40	231-239	
		QGLLPVLESFK	53	237-247	
		QKLHELQE K (E → pyroglutamic acid)	46	240-250	
		VEPLRAELQE GAR	54	156-164	
		LLDNWDSVTSTFSK	47	143-155	
		DEPPQSPPWDR + 1 Oxidation (W)	43	70-83	
		DLATVYVDVLK	55	25-34	
		VSFLSALEEEYTK	53	37-47	
		KWQEEMELYR + 1 Oxidation (M)	56	251-262	
			57	131-140	

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Spot exp1	Spot exp2	Peptide	Seq ID No.	aa	Identification in database	ID number database
4310	144	THLAPYSDELR	42	185-195	Apolipoprotein A-I	P02647
4606+4605	143	THLAPYSDELR LGEVNTYAGDLQK LLPHANEVSQK QLTPYAQR IDQNVEELKGR LTPYADEFK ISASAEELR LAPLAEDVR ALVQQMEQLR + 1 Oxidation (M)	42 58 59 60 61 62 63 64 65	185-195 66-78 113-123 156-163 190-200 201-209 256-264 267-275 135-143	Apolipoprotein A-I Apolipoprotein A-I Apolipoprotein A-IV	P02647 P02647 P06727
5402	81	LEPYADQLR IDQNVEELKGR LTPYADEFK IDQTVEELR ISASAEELR LAPLAEDVR ALVQQMEQLR + 1 Oxidation (M) RVEPYGENFNK SLAPYAQDTQEK LGEVNTYAGDLQK KVEQAVETEPEPELR AYKSELEEQQLTPVAEETR LSKELQAAQAR AATVGSLAGQPLQER AKLEEQAQQIR LQAEAFQAR LQAEAFQAR AKLEEQAQQIR	66 61 62 67 63 64 65 68 69 58 4 11 12 7 2 1 1 2	190-200 201-209 212-220 257-264 267-275 317-326 306-317 222-233 66-78 19-33 91-109 111-121 210-224 259-269 270-278 270-278 259-269	Apolipoprotein A-IV	P06727
5502	110				Apolipoprotein E	P02649

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Spot exp1	Spot exp2	Peptide	Seq ID No.	aa	Identification in database	ID number database
		LLRIDADDLQK KVEQAVETEPEPELR	3	166-175 19-33		
114		LQAEAFQAR AKLEEQQQQR LGPLVEQGR VQAAVGTSAAAPVPSDNH LGPLVEQGR LGPLVEQGR KVEQAVETEPEPELR LQAEAFQAR LGPLVEQGR AKLEEQQQQR ALMDDETMKELK + 2 Oxidations (M)	4 1 2 6 5 5 4 1 5 2	270-278 259-269 199-207 301-317 199-207 199-207 19-33 270-278 199-207 259-269	Apolipoprotein E Apolipoprotein E Apolipoprotein E Apolipoprotein E Apolipoprotein E Apolipoprotein E Apolipoprotein E Apolipoprotein E Apolipoprotein E	P02649 P02649 P02649 P02649 P02649 P02649 P02649 P02649 P02649
272	862		70	80-90		
681	480		71	326-336	Apolipoprotein J	P10909
3405	3505	ELDESLSQVAER ELDESLSQVAER ELDESLSQVAER KYNELLK	71	326-336	Apolipoprotein J	P10909
4401	323		71	326-336	Apolipoprotein J	P10909
5302	108	FMETVAEK + 1 Oxidation (M) ELDESLSQVAER EILSVDCTNNPSQAK + 1 (cys-CAM) TLLSNLEAK	73 71 74 75	430-437 326-336 307-322 69-78	Apolipoprotein J Apolipoprotein J	P10909
8601		IDSLENDR ASSIDELFQDR AGALNSNDAFVLK YIETDPANR AGALNSNDAFVLK TGAQELLR TEGDGVYTNDKK	76 77 78 79 78 80 81	159-167 183-194 585-597 730-738 585-597 616-623 60-72	Gelsolin Gelsolin Gelsolin Haptoglobin-1/2	P06396 P06396 P00737

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Spot exp1	Spot exp2	Peptide	Seq ID No. aa	Identification in database	ID number database
		TEGDGVYTLLNDKKQWINK + 1 ox (W)	82 119-131 60-77		P00738 P00737
5903RBH		NFPSPVDAAFR GGYTLVSGYPK	83 84 92-102 333-343	Hemopexin	P00738 P02790
8902RBH		NFPSPVDAAFR QGHNSVFLIK	83 85 92-102 103-112	Hemopexin	P02790
		DYFMPCPGK + 1 (cys-CAM + ox) + 1 ox (M)	86 226-234		
4701RBH		GGYTLVSGYPK SAVQGP PER	84 87 333-343 169-177	Ig alpha-1 chain C region (heavy)	P01876
4804		QEPSQGTTFAVTSILR TPLTATLSK	88 89 283-299 213-221	Ig alpha-1 chain C region (heavy)	P01876
4702		TVGSDDTFYSFK QVVAGLNFR YFDFFVAR	90 91 65-75 188-196	Kininogen	P01042
8101		APEAQVSVQPNFQQDK	92 93 317-324 23-38	Prostaglandin-H2 D- isomerase	P41222
9209		TMLLQPAGSLGSYSYR + 1 Oxidation (M) AQGFTEDTIVFLPQTDK [1617.85] <sup>+</sup> EAQVSVQPNF[518.26] <sup>+</sup>	94 95 96 93-108 169-185 23-38	Prostaglandin-H2 D- isomerase	P41222
6001		TMLLQPAGSLGSYSYR + 1 Oxidation (M) AADDTDEPFASGK (aa 61 : W → D)	94 97 93-108 56-68		P02766
7102		[603.41]PLMVK	98 21-35	Transthyretin	P02766
7108	274	GPTGTGESKCPLMVK (Cys(O <sub>3</sub> H))	99 21-35	Transthyretin	P02766

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		GPTGTGESKCPPLMVK (Cys(O <sub>3</sub> H) <sub>Y/M</sub> : oxidation to sulfone)	99	21-35		
		AADDTWEPEFASGK (W + 2*16 Da)	100	56-68		
		AADDTDEPFASGK (aa 61 : W → D)	97	56-68		
		AADDTWEPEFASGK	100	56-68		
		KAADDTWEPEFASGK	102	55-68		
		TSESGELHGLTTTEEFVEGIYK	103	69-90		
		HLSLLTTLNSR	104	208-218	Vitamin D-binding protein	P02774
		YTFELSR	105	346-352		
		THLPEVFLSK	106	354-363		
		VLEPTLK	107	364-370		
		ELSSFIDK	108	395-402		
		VCQYAAAYGEK (cys-CAM + ox)	109	219-229	Vitamin D-binding protein	P02774
		VMDKYTFELSR + 1 Oxidation (M)	110	342-352		
		YTFELSR	105	346-352		
		THLPEVFLSK	106	354-363		
		VLEPTLK	107	364-370		
		[1433_61] <sup>†</sup> CCDVVEDSTTCFNAK (1 cys-CAM + ox, 2 Dha)	111	371-388		
		ELSSFIDK	108	395-402		
		AKLPDATPK	112	428-436		
		AGEVQEPELR	113	239-248	Zinc-alpha-2-glycoprotein	P23311
		QDPPSVVVTSHQAPGEK	101	201-217		
3601RBH						
4411						
2402	88					